R Basics

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What is R?

- R is statistical numerical software
- R is a "dialect" of the S statistical programming language
- R is a system for interactive data analysis
- R is a high-level programming language
- R is free
- R is state-of-the-art in statistical computing. It is what many (most?) research statisticians use in their work

Why Use R?

- R is FREE! That, by itself, is almost enough. No complicated licensing. Broad dissemination of research methodologies and results, etc.
- R is available for a variety of computer platforms (e.g., Linux, MacOS, Windows).
- R is widely used by professional statisticians, biologists, demographers, and other scientists. This increases the likelihood that code will exist to do a calculation you might want to do.
- R has remarkable online help lists, tutorials, etc.
- R represents the state-of-the-art in statistical computing.

But Wouldn't Something Menu-Driven Be *Easier*?

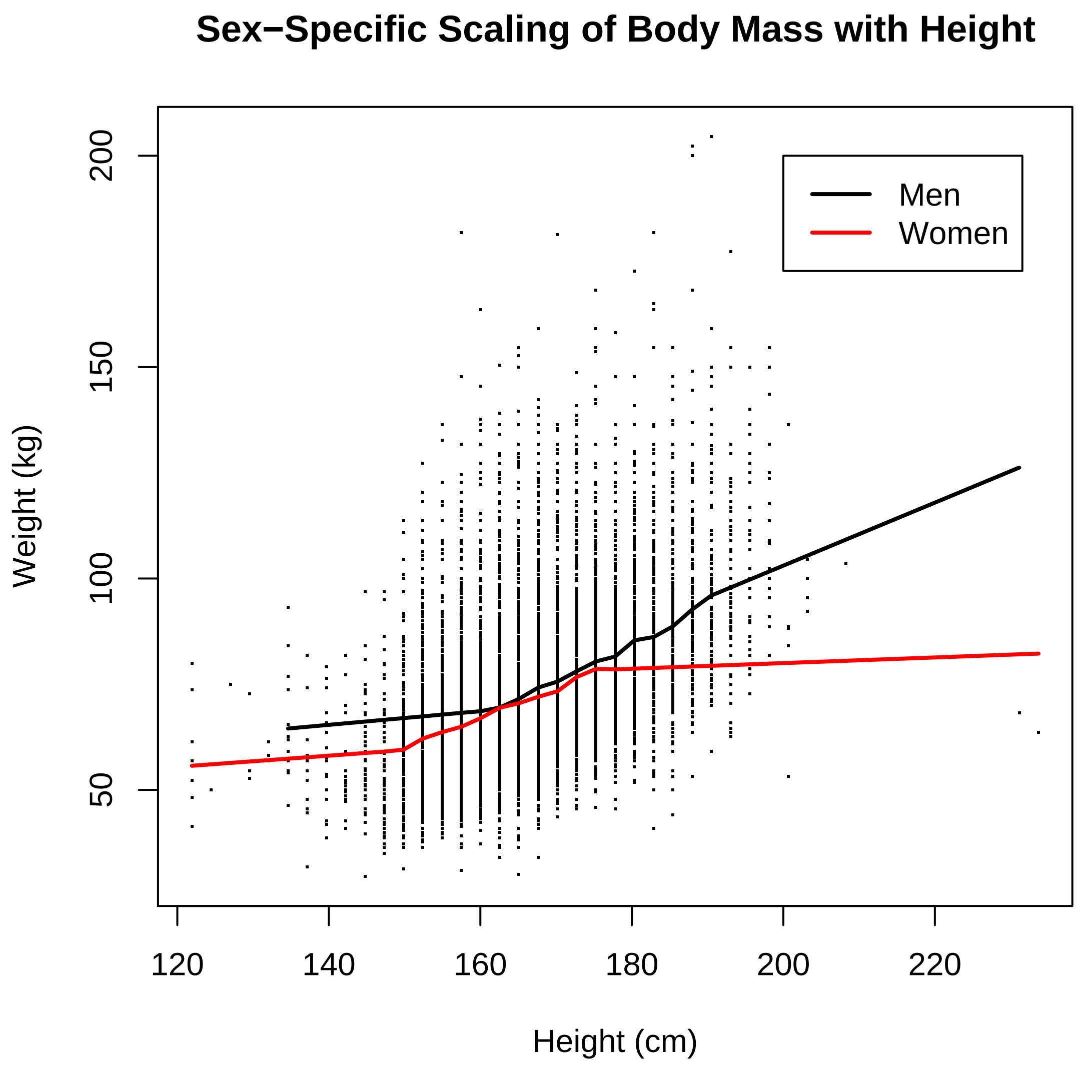
Fallacious thinking

- For teaching, text-based input is always better
- Example code can be copied and input *exactly*; you can then tweak it and see what happens, facilitating the learning process

Here's an example

Consider the following absurdly complex graphic which plots body mass values against height for nearly 20,000 individuals sampled in the 2000 NHANES survey

In addition to plotting the raw values, it draws smooth curves for men and women through the data cloud


Sex−Specific Scaling of Body Mass with Height
Men
Women
Weight (kg)
Height (cm)
50
100
150
200
120
140
160
180
200
220

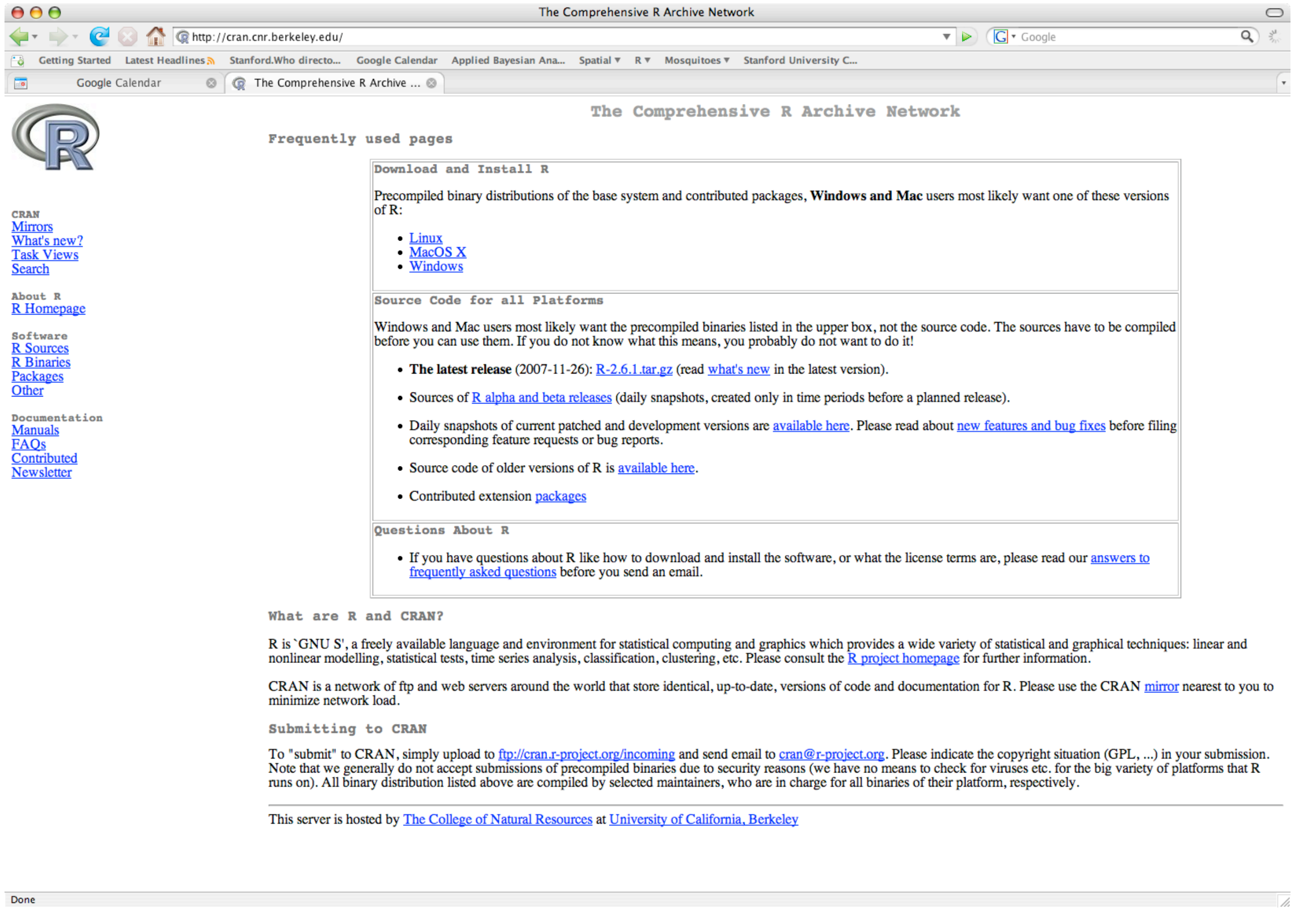
How Do I Get R?

R is distributed via the Comprehensive R Archive Network (CRAN)

The general URL for CRAN is: http://www.r-project.org

The closest CRAN mirror is hosted in Berkeley: http://cran.cnr.berkeley.edu/

The Berkeley CRAN Mirror



The Comprehensive R Archive Network

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Mirrors
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Task Views
Search

About R
R Homepage

Software
R Sources
R Binaries
Packages
Other

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FAQs
Contributed
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Frequently used pages

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- Linux
- MacOS X
- Windows

Source Code for all Platforms

Windows and Mac users most likely want the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- **The latest release** (2007-11-26): R-2.6.1.tar.gz (read what's new in the latest version).
- Sources of R alpha and beta releases (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are available here. Please read about new features and bug fixes before filing corresponding feature requests or bug reports.
- Source code of older versions of R is available here.
- Contributed extension packages

Questions About R

- If you have questions about R like how to download and install the software, or what the license terms are, please read our answers to frequently asked questions before you send an email.

What are R and CRAN?

R is `GNU S', a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the R project homepage for further information.

CRAN is a network of ftp and web servers around the world that store identical, up-to-date, versions of code and documentation for R. Please use the CRAN mirror nearest to you to minimize network load.

Submitting to CRAN

To "submit" to CRAN, simply upload to ftp://cran.r-project.org/incoming and send email to cran@r-project.org. Please indicate the copyright situation (GPL, ...) in your submission. Note that we generally do not accept submissions of precompiled binaries due to security reasons (we have no means to check for viruses etc. for the big variety of platforms that R runs on). All binary distribution listed above are compiled by selected maintainers, who are in charge for all binaries of their platform, respectively.

This server is hosted by The College of Natural Resources at University of California, Berkeley

Calculations

Dalgaard (2002) refers to R as “an overgrown calculator”

R can indeed be used to do simple calculations

```
> # addition
> 2+2
[1] 4
> # multiplication
> 2*3
[1] 6
> a <- 2
> b <- 3
> a*b
[1] 6
> # division
> 2/3
[1] 0.6666667
> b/a
[1] 1.5
> 1/b/a
[1] 0.1666667
> # note precedence!
> 1/(b/a)
[1] 0.6666667
> # parentheses can override precedence
> # an exponential
> exp(-2)
[1] 0.1353353
> # why we age
> r <- 0.02
> exp(-r*45)
[1] 0.4065697
> # something more tricky
> exp(log(2))
[1] 2
```

The numbers before the output indicate which element of a vector the line starts with

```
> # generate 20 normally distributed random numbers
> rnorm(20)
 [1]  1.33388612 -0.14253810 -1.42411986  1.55193795 -0.72119736  0.67747616
 [7] -0.99163230  1.49105307  0.73801860 -0.42041627 -0.40124719 -0.20960572
[13] -0.51279375  0.85793076  0.12453478  0.73358344 -1.17897816 -1.04913413
[19]  0.06780631 -0.76912890
```

Inputting Data

Most operations in R take the form

$$\texttt{lhs} \leftarrow \texttt{rhs}$$

using the assignment operator, `<-`

Note that this assignment is different from mathematical equality (something that can trip up beginners)

This means that it's perfectly acceptable to assign something to itself in changed form (we'll see this, e.g., when we create matrices)

In R versions 2.+, you can actually use `=`. I'm old-school, so don't expect to see this from me...

Data are input interactively by concatenating values using a comma-delimited list:

```
> ages <- c(0,5,10,15,20)
```

This applies to lists of text values as well:

```
> factors <- c("male","female","other")
```

Some Data Types

Numeric: All numbers in R are of the form double

Factor: For categorical data

```
> countries <- factor(c("colombia", "ecuador", "mexico", "brazil"))
> countries
[1] colombia ecuador  mexico   brazil
Levels: brazil colombia ecuador mexico
```

Notice that factors are printed without the quotes. This is because R stores them as a set of codes

Use this trick to get some insight into how factors are handled by R:

```
> unclass(countries)
[1] 2 3 4 1
attr(,"levels")
[1] "brazil"   "colombia" "ecuador"  "mexico"
```

Another important type of vector is a logical vector

```
> t.or.f <- c(T,F,F,T,T)
> is.logical(t.or.f)
[1] TRUE
```

You can mix different types of data in a list using the command `list()`

```
child1 <- list(name="mary", child.age=6,
status="foster",mother.alive=F, father.alive=T, parents.ages=c(24,35))
```

This is useful when you write your own functions and want to output multiple things

Data Frames

A data frame is an R object which stores a data matrix

A data frame is essentially a list of variables which are all the same length

A single data frame can hold different types of variables

A nice demographic example is a life table

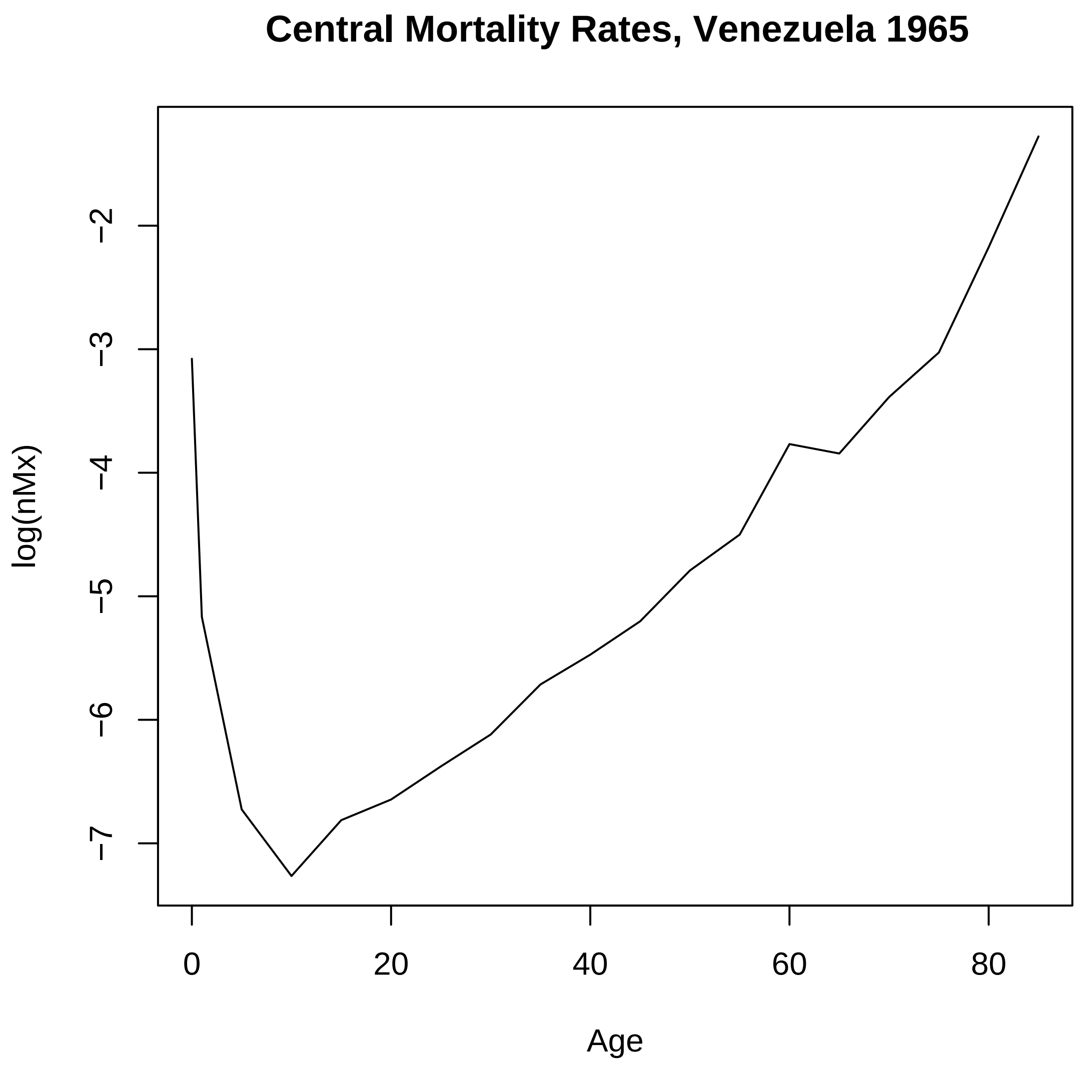
A Data Frame

```
> vlt <- read.table("/Users/jhj1/Teaching/summercourse/rdemog/venezuela1965.lifetable.txt", header=TRUE)
> vlt
    x    nax    nMx    nqx     lx    ndx    nLx    Tx    ex
1   0 0.1483 0.0461 0.0443 1.0000 0.0443 0.9622 67.70 67.70
2   1 1.5000 0.0057 0.0226 0.9557 0.0216 3.7687 66.74 69.84
3   5 2.5000 0.0012 0.0058 0.9341 0.0055 4.6568 62.97 67.41
4  10 2.5000 0.0007 0.0036 0.9286 0.0034 4.6347 58.31 62.80
5  15 2.5000 0.0011 0.0054 0.9253 0.0050 4.6138 53.68 58.01
6  20 2.5000 0.0013 0.0065 0.9202 0.0060 4.5863 49.07 53.32
7  25 2.5000 0.0017 0.0086 0.9143 0.0079 4.5516 44.48 48.65
8  30 2.5000 0.0022 0.0109 0.9064 0.0098 4.5074 39.93 44.05
9  35 2.5000 0.0033 0.0163 0.8966 0.0146 4.4463 35.42 39.51
10 40 2.5000 0.0042 0.0209 0.8820 0.0184 4.3639 30.97 35.12
11 45 2.5000 0.0055 0.0273 0.8636 0.0236 4.2588 26.61 30.81
12 50 2.5000 0.0083 0.0406 0.8400 0.0341 4.1146 22.35 26.61
13 55 2.5000 0.0111 0.0542 0.8059 0.0436 3.9202 18.24 22.63
14 60 2.5000 0.0231 0.1090 0.7622 0.0831 3.6035 14.32 18.78
15 65 2.5000 0.0214 0.1015 0.6792 0.0689 3.2235 10.71 15.77
16 70 2.5000 0.0338 0.1558 0.6103 0.0951 2.8136  7.49 12.27
17 75 2.5000 0.0485 0.2164 0.5152 0.1115 2.2971  4.68  9.08
18 80 2.5000 0.1137 0.4426 0.4037 0.1787 1.5717  2.38  5.89
19 85 3.5868 0.2788 1.0000 0.2250 0.2250 0.8070  0.81  3.59
```

Accessing Data Frame Elements

To access a variable contained in a data frame, use the data frame name followed by the variable name, separated by a dollar sign, $

```
> vlt$lx
 [1] 1.0000 0.9557 0.9341 0.9286 0.9253 0.9202 0.9143 0.9064 0.8966 0.8820
[11] 0.8636 0.8400 0.8059 0.7622 0.6792 0.6103 0.5152 0.4037 0.2250
> plot(vlt$x, log(vlt$nMx), type="l", xlab="Age", ylab="log(nMx)")
> title("Central Mortality Rates, Venezuela 1965")
```



Central Mortality Rates, Venezuela 1965
log(nMx)
−2
−3
−4
−5
−6
−7
0
20
40
60
80
Age

Creating Data Frames

```
> x1 <- rnorm(10)
> x2 <- rpois(10,3)
> x3 <- rgamma(10, shape=2, scale=10)
> random.numbers <- data.frame(norm=x1, poisson=x2, gamma=x3)
> random.numbers
          norm poisson     gamma
1   1.04016722       2 18.024196
2  -0.19090848       2 26.040085
3  -0.94342252       4 10.559723
4   2.03184242       3 10.444649
5   0.84143037       2  5.793161
6  -0.82939271       4 30.909734
7   0.96106259       2 13.797753
8  -0.36066836       3  7.428749
9   1.05773152       2 15.142058
10  0.07456312       5 34.357035
```

Creating Vectors

You frequently don't want to input the values of a vector manually

We frequently want either regularly spaced vectors (e.g., ages) or a vector of, say, one value repeated

R has a number of facilities to perform these operations

```
> count <- 1:20
> count
 [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20

> ages <- seq(0,85,by=5)
> ages
 [1]  0  5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85

> ones <- rep(1,10)
> ones
 [1] 1 1 1 1 1 1 1 1 1 1

> rep(c(1,2),c(5,10))
 [1] 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2
```

Reading Data

There are a number of ways to read data into R

Probably the easiest and most frequently used involves reading data from plain-text (ascii) files

These files can be space, tab, or comma delimited

You can create these files in a spreadsheet program like Excel or output them from most standard statistical packages

```
> vlt <- read.table("venezuela1965.lifetable.txt", header=TRUE)
```

Here are the elements:

- `vlt`: this is the name you call your newly read-in data frame
- Whole data sets in R (data frames) are stored as variables – this allows you to have multiple datasets available at the same time
- `<-` This is the assignment operator. In R 2.+, you can use an equals sign, but don't expect that out of me!

- `read.table` is the command to read a table
- Give it the file name enclosed in double quotes – you don't need the full path if the file is in your working directory
- `header=TRUE` tells R that the first row contains column names. It's almost always a good idea to specify this
- There are several other optional arguments that I left out
- Some important ones are: `skip=n` which tells R to ignore the first `n` lines of the file (which may be a header, comments or a description of the file) and `sep` which tells R explicitly what separates columns (`"\t"` is tab)

More on Reading Data

R assumes that your data are space delimited when you use `read.table()`

If your file is delimited by something other than spaces, it is a good idea to use a slightly different function

```
> quercus <- read.delim("quercus.txt", skip=24, sep="\t", header=TRUE)
```

Note this time I used `skip=24` and `sep="\t"`

Bonus points if you can tell me what *Quercus* is...

Reading Binary Data Files

R has its own binary data format

Files end with the extension `.RData`

Use the command `load()` to read in R binary data files

```
> load("body.size.RData")
```

These can be big so watch out

You can access built-in data sets using the command `data()`

```
> data(cars)
```

Use the command with no arguments to find out what data files are available to you

```
> data()
```

Reading Data From Other Statistical Packages

R has a package called `foreign` which provides functions for reading binary data from a wide variety of statistical packages

Some very useful ones include `read.sta` for reading Stata binary files and `read.sps` for reading SPSS files and `read.xport` for reading SAS export files

R has facilities for interfacing with SQL databases, which is very handy when you work with large databases

Exploring Your Data

Once you've read the data in, you might want to get some information about the dataset (e.g., variable names, their distributions, etc.)

Use the `summary()` function to do this

```
> quercus <- read.delim("quercus.txt", skip=24, sep="\t",header=TRUE)
>  summary(quercus)
                          Species              Region          Range        
 Quercus Chapmanii Sarg.       : 1   Atlantic   :28   Min.    :   13.0  
 Quercus Douglasii Hook. & Arn: 1   California:11   1st Qu.:  827.5  
 Quercus Durandii Buckl.       : 1                   Median : 5328.0  
 Quercus Engelmannii Greene    : 1                   Mean   : 7882.6  
 Quercus Garryana Hook.        : 1                   3rd Qu.:11924.5  
 Quercus Kelloggii Newb.       : 1                   Max.   :28389.0  
 (Other)                       :33                                    
   acorn.size       tree.height   
 Min.   : 0.300   Min.   : 0.30  
 1st Qu.: 1.100   1st Qu.:10.00  
 Median : 1.800   Median :18.00  
 Mean   : 3.341   Mean   :17.34  
 3rd Qu.: 4.450   3rd Qu.:24.00  
 Max.   :17.100   Max.   :30.00  
```

The Working Directory

Something that almost invariably messes up novice users is the idea of a **working directory**

The working directory is the directory from which R was launched

Unless you specify a path explicitly, this is where R will look for files (e.g., data you are trying to load, code you are sourcing, etc.)

You can figure out what your working directory is by the command `getwd()`

Once you know what this is, you can move relevant files there using the finder or a shell

In the Mac RGui, there is a status bar that tells you what your working directory is

Sometimes you want to change your working directory (I almost always do when I use the Mac RGui)

Use the command `setwd()` to change your working directory

Under the Mac RGui, you can also use command-D (use command on the Misc menu)

```
> getwd()
[1] "/Users/jhj1"
> setwd("/Users/jhj1/Teaching/space/workshop08/")
> getwd()
[1] "/Users/jhj1/Teaching/space/workshop08"
```

The Workspace

R handles data in a manner that is different than many statistical packages

In particular, you are not limited to a single rectangular data matrix at a time

The workspace holds all the objects (e.g., data frames, variables, functions) that you have created or read in

You can essentially have as many data frames as your machine's memory will allow

To find out what lurks in your workspace, use `objects()` command

```
> objects()
 [1] "age"            "hort"           "life.table"     "mad.bx"
 [5] "mad.nDx"        "mad.nKx"        "random.numbers" "usa.bx"
 [9] "usa.nDx"        "usa.nKx"        "ven.bx"         "ven.nDx"
[13] "ven.nKx"        "vlt"            "x1"             "x2"
[17] "x3"
```

To remove an object, use `rm()`

```
> rm(x3)
> objects()
 [1] "age"            "hort"           "life.table"     "mad.bx"
 [5] "mad.nDx"        "mad.nKx"        "random.numbers" "usa.bx"
 [9] "usa.nDx"        "usa.nKx"        "ven.bx"         "ven.nDx"
[13] "ven.nKx"        "vlt"            "x1"             "x2"
```

If you *really* want to clear your whole workspace, use the following

```
> rm(list=ls())
```

Beware. Once you do this, you don't get the data back

Subsetting

Access the elements of a data frame using the dollar sign:

```
> quercus$acorn.size
 [1]  1.4  3.4  9.1  1.6 10.5  2.5  0.9  6.8  1.8  0.3  0.9  0.8  2.0  1.1  0.6
[16]  1.8  4.8  1.1  3.6  1.1  1.1  3.6  8.1  3.6  1.8  0.4  1.1  1.2  4.1  1.6
[31]  2.0  5.5  5.9  2.6  6.0  1.0 17.1  0.4  7.1
>
```

Subsetting anything other than a data frame uses square brackets

```
> size <- quercus$acorn.size
> # first 3 elements
> size[1:3]
[1] 1.4 3.4 9.1
> # element 17
> size[17]
[1] 4.8
> # all but the last
> size[-39]
 [1]  1.4  3.4  9.1  1.6 10.5  2.5  0.9  6.8  1.8  0.3  0.9  0.8  2.0  1.1  0.6
[16]  1.8  4.8  1.1  3.6  1.1  1.1  3.6  8.1  3.6  1.8  0.4  1.1  1.2  4.1  1.6
[31]  2.0  5.5  5.9  2.6  6.0  1.0 17.1  0.4
> # elements 3,6,9
> size[c(3,6,9)]
[1] 9.1 2.5 1.8
> # using a logical
> # note this uses one of the variables in the data frame "quercus"
> # to subset the vector we extracted
> size[quercus$Region=="California"]
 [1]  4.1  1.6  2.0  5.5  5.9  2.6  6.0  1.0 17.1  0.4  7.1
> # access an element of an array or data frame by X[row,col]
> quercus[3,4]
[1] 9.1
# for data frames with named columns, access by col name
> quercus[,"tree.height"]
 [1] 27.0 21.0 25.0  3.0 24.0 17.0 15.0  0.3 24.0 11.0 15.0 23.0 24.0  3.0 13.0
[16] 30.0  9.0 27.0  9.0 24.0 23.0 27.0 24.0 23.0 18.0  9.0  9.0  4.0 18.0  6.0
[31] 17.0 20.0 30.0 23.0 26.0 21.0 15.0  1.0 18.0
>
```

The comma with nothing in front of it means take every row in the the column named `"tree.height"`

Subsetting Notes

positive indices include, negative indices exclude elements

`1:3` means a sequence from 1 to 3

You can only use a single negative subscript, i.e., you can't use `quercus$acorn.size[-1:3]`

Of course, you can get around this by enclosing the vector in parentheses `quercus$acorn.size[-(1:3)]`

To test for equality, you need to equals signs ==

When you refer to a variable in a data frame, you must specify the data frame name followed a dollar sign and the variable name `quercus$acorn.size`

Subsetting with Logicals

Testing for equality is just a special case of a logical test

Missing Values

`NA` is a special code for missing data.

`NA` pretty much means “Don’t Know”

The presence of `NA`s in your dataset can lead to some surprising consequences when you work with it

You can’t test for a `NA` the way you would test for any other value (i.e., using the == operator) since `variable==NA` is like asking in English, is the variable equal to some number I don’t know? How could you know that?!

R therefore provides the function `is.na()`

Creating Lists, Vectors, and Matrices

c() concatenates a list of items

- You use this a lot
- It's a common mistake to forget the c() when putting together a list of numbers, factors, etc.
- If you do forget it, you will get a syntax error

```
# a list of numbers
> x <- c(1,2,3,4,5)
> x
[1] 1 2 3 4 5
>  col <- c("black","red","green")
> col
[1] "black" "red"   "green"
> # concatenating 2 lists
> x1 <- c(7,8,9)
> y <- c(x,x1)
> y
[1] 1 2 3 4 5 7 8 9
> # don't forget the 6!
> y <- c(x,6,x1)
> y
[1] 1 2 3 4 5 6 7 8 9
```

sequences are formed with `seq()`

```
>  x <- seq(0,10)
> x
 [1]  0  1  2  3  4  5  6  7  8  9 10
> # use the optional by= argument to specific the interval between items
> x <- seq(0,10,by=2)
> x
[1]  0  2  4  6  8 10
> # use length= to specify a fixed length and let R figure out the interval lengths
> x <- seq(0,1,length=23)
> x
 [1] 0.00000000 0.04545455 0.09090909 0.13636364 0.18181818 0.22727273
 [7] 0.27272727 0.31818182 0.36363636 0.40909091 0.45454545 0.50000000
[13] 0.54545455 0.59090909 0.63636364 0.68181818 0.72727273 0.77272727
[19] 0.81818182 0.86363636 0.90909091 0.95454545 1.00000000
> # this is often useful for plotting functions
```

Sometimes you want to repeat a value or set of values – this is useful if your setting up a dataset and want to repeat factors

```
> rep(2,10)
 [1] 2 2 2 2 2 2 2 2 2 2
> rep(c(1,2),10)
 [1] 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2
> rep(c(1,2),c(10,10))
 [1] 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2
> rep("R roolz!",3)
[1] "R roolz!" "R roolz!" "R roolz!"
>
```

A vector is a list of numbers – it turns out everything in R is represented as a vector but that doesn't affect your life much

Create a vector using one of the techniques we just discussed

A matrix is a rectangular array of numbers – it is a vector of vectors, with the numbers indexed by row and column

One way to create matrices is to "bind" columns together using the command `cbind()` (or `rbind`)

```
> cx1980 <- c(7, 13, 8, 13, 5, 35, 9)
> cx1988 <- c(9, 11, 15, 8, 9, 38, 0)
> C <- cbind(cx1980, cx1988)
> C
     cx1980 cx1988
[1,]      7      9
[2,]     13     11
[3,]      8     15
[4,]     13      8
[5,]      5      9
[6,]     35     38
[7,]      9      0
>
```

What would happen if I instead typed `C <- c(cx1980, cx1988)` ?

```
>  C <- c(cx1980, cx1988)
> C
 [1]  7 13  8 13  5 35  9  9 11 15  8  9 38  0
>
```

Not a matrix, but we can make it one...

```
> C <- matrix(C,nrow=7,ncol=2)
> C
     [,1] [,2]
[1,]    7    9
[2,]   13   11
[3,]    8   15
[4,]   13    8
[5,]    5    9
[6,]   35   38
[7,]    9    0
>
```

What happens if we try to bind columns of different lengths

```
> cx.boesch <- c(18,10,15,30)
> C <- cbind(C,cx.boesch)
Warning message:
number of rows of result
is not a multiple of vector length (arg 2) in: cbind(1, C, cx.boesch)
> C
           cx.boesch
[1,]  7  9        18
```

```
[2,] 13 11        10
[3,]  8 15        15
[4,] 13  8        30
[5,]  5  9        18
[6,] 35 38        10
[7,]  9  0        15
>
```

Both the warning message and the output can seem a little odd to the uninitiated

```
> a <- c(2,4)
> b <- c(1,3,1,3)
> cbind(a,b)
     a b
[1,] 2 1
[2,] 4 3
[3,] 2 1
[4,] 4 3
```

R uses a recycling rule for filling out vectors and matrices – when you try to put together things that are neither the same length nor multiples of each other, you get a warning

Use the recycling rule to make a matrix of ones

```
> x <- matrix(1,nr=3,nc=3)
> x
```

```
     [,1] [,2] [,3]
[1,]    1    1    1
[2,]    1    1    1
[3,]    1    1    1
>
```

Note that using the short version of `nrow`, `nr`, is sufficient. This is often true – you can use the minimum name that is unambiguous

Add-On Packages

One of the great advantages of R is all the user-contributed packages. Frequently, these packages are written by the people who invent the technique!

R version 2.+ uses a graphical package manager for most (all?) platforms – it is pretty self-explanatory

In order to use an R package in a work session, you use the command `library()`

```
> library(survival)
Loading required package: splines
>
```

Sometimes you will get a message (as you do for `survival`), sometimes you won't

You need to load the package every time you start a new R session

Find out from the command line what packages are available:

```
> library()
Packages in library '/Library/Frameworks/R.framework/Resources/library':

AnnBuilder              Bioconductor annotation data package builder
Biobase                 Biobase: Base functions for Bioconductor
Biostrings              String objects reepresenting biological
                        sequences
Category                Category Analysis
ChromoViz               Multimodal visualization of gene expression
                        data
CoCiteStats             Different test statistics based on co-citation.
DEDS                    Differential Expression via Distance Summary
                        for Microarray Data
DNAcopy                 DNA copy number data analysis
DynDoc                  Dynamic document tools
EBarrays                Empirical Bayes for Microarrays
Epi                     A package for statistical analysis in
                        epidemiology.
GRASS                   Interface between GRASS 5.0 geographical
                        information system and R
ISwR                    Introductory Statistics with R
KernSmooth              Functions for kernel smoothing for Wand & Jones
                        (1995)
MASS                    Main Package of Venables and Ripley's MASS
UsingR                  Data sets for the text "Using R for
                        Introductory Statistics"
ade4                    Analysis of Environmental Data : Exploratory
                        and Euclidean methods in Environmental sciences
.
.
.
```

Vectorized Calculation

We frequently want to perform arithmetic operations on lists

This is easy to do in R

A simple model for the annual rate of increase for an iteroparous organism is

$$\lambda = s + b$$

where s is the average annual survival probability, and b is the average fertility of each adult

Given some values of s and b, we can calculate λ

```
> s <- c(0.9544535, 0.9424282, 0.9416734, 0.9338940, 0.9195420,
0.9509079, 0.9561570, 0.9641317, 0.9071128, 0.9448746)

> b <- c(0.044712181, 0.051761901, 0.055269254, 0.009568243,
0.084174678, 0.037728583, 0.100465837, 0.055931991, 0.068072939,
0.015960763)

> lambda <- s+b
> lambda
 [1] 0.9991657 0.9941901 0.9969426 0.9434622 1.0037167 0.9886365 1.0566229
 [8] 1.0200637 0.9751857 0.9608354
```

Some funny things can happen with vectorized arithmetic, so beware

What happens here?

```
> a <- c(1,2,3,4)
> b <- c(5,7)
> c <- a+b
```

But if we try this:

```
> b <- c(5,7,9)
> c <- a+b
Warning message:
longer object length
is not a multiple of shorter object length in: a + b
```

This trick results from R's **recycling rule**

A Funky Bit of R Syntax

The value of this function is not likely to be immediately apparent

I will nonetheless present it anyway since I am likely to use it, so you should know what I'm doing

R, like any other computational environment, has *scope* rules.

Scope describes the range in a program where a variable or function is visible and accessible

Variable names in data frames are not immediately available to the workspace – you have to use the data frame name - dollar sign - variable name syntax

Sometimes this can be cumbersome and R allows you to set up a temporary local environment that allows you to call variable names without the data frame names

```
> load("/Users/jhj1/Teaching/a192/datasets/body.size.RData")
> with(body.size, plot(height[sex==1],weight[sex==1], xlab="Height (in)", ylab="Weight (lbs)"))
```

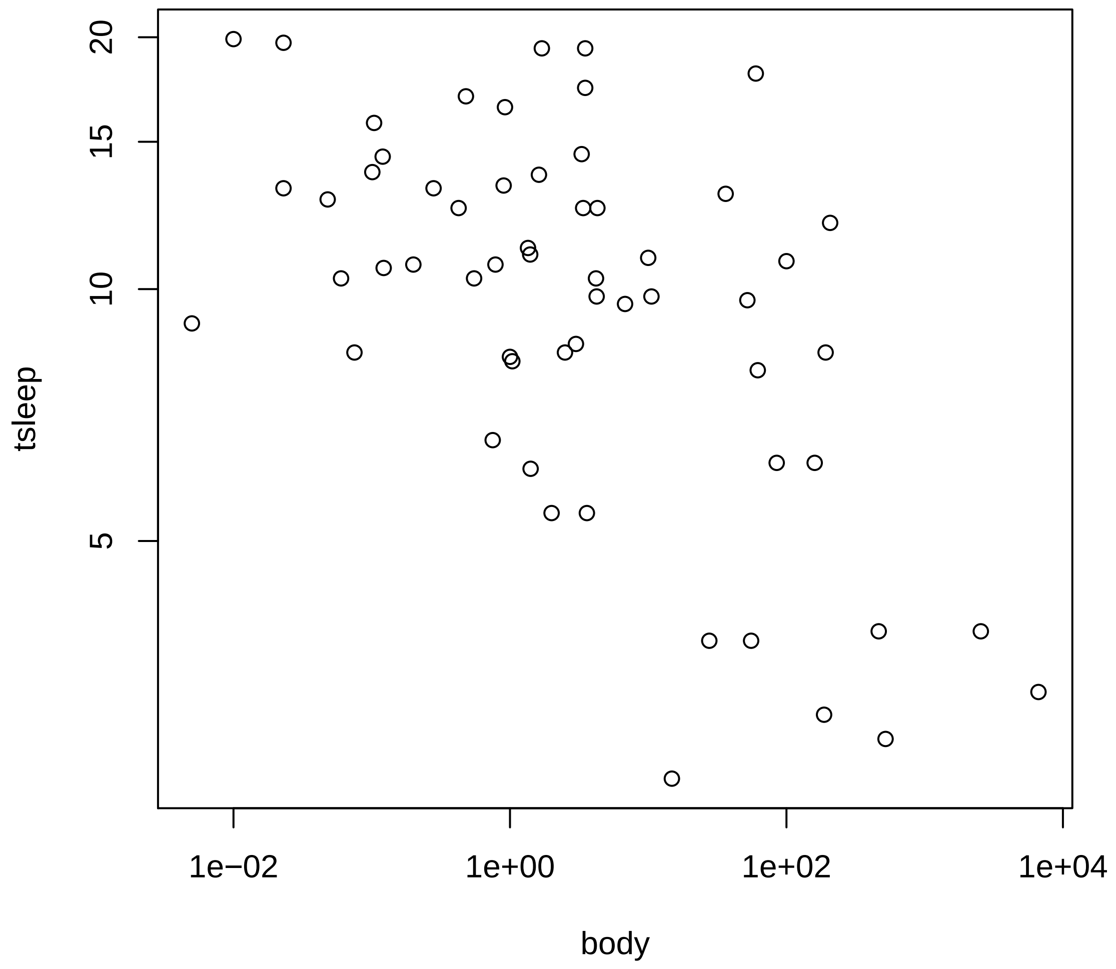
`with()` essentially says: use this dataset for everything enclosed in these parentheses

Bivariate Plots

Do big mammals sleep more than little mammals?

```
sleep <- read.table("/Users/jhj1/Teaching/a192/datasets/sleep.data.dat",header=TRUE)
with(sleep, plot(body,tsleep,log="xy"))
```

Nope

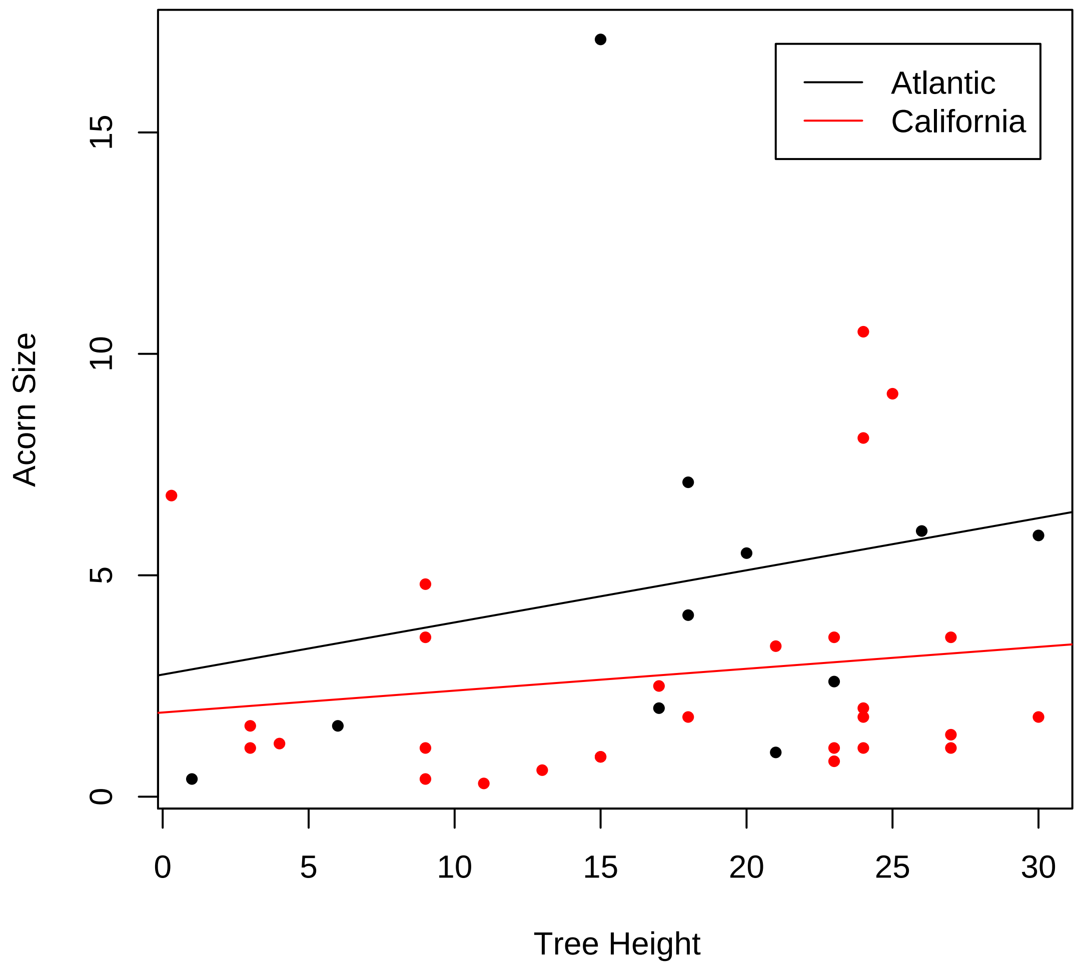


More Bivariate Plots

Here is a pretty complicated plot of Acorn size vs. tree height in two biogeographically distinct groups of oaks

This is the sort of plot we would want to construct to evaluate the hypothesis that relative acorn size in Californian oaks is smaller than in Atlantic oaks

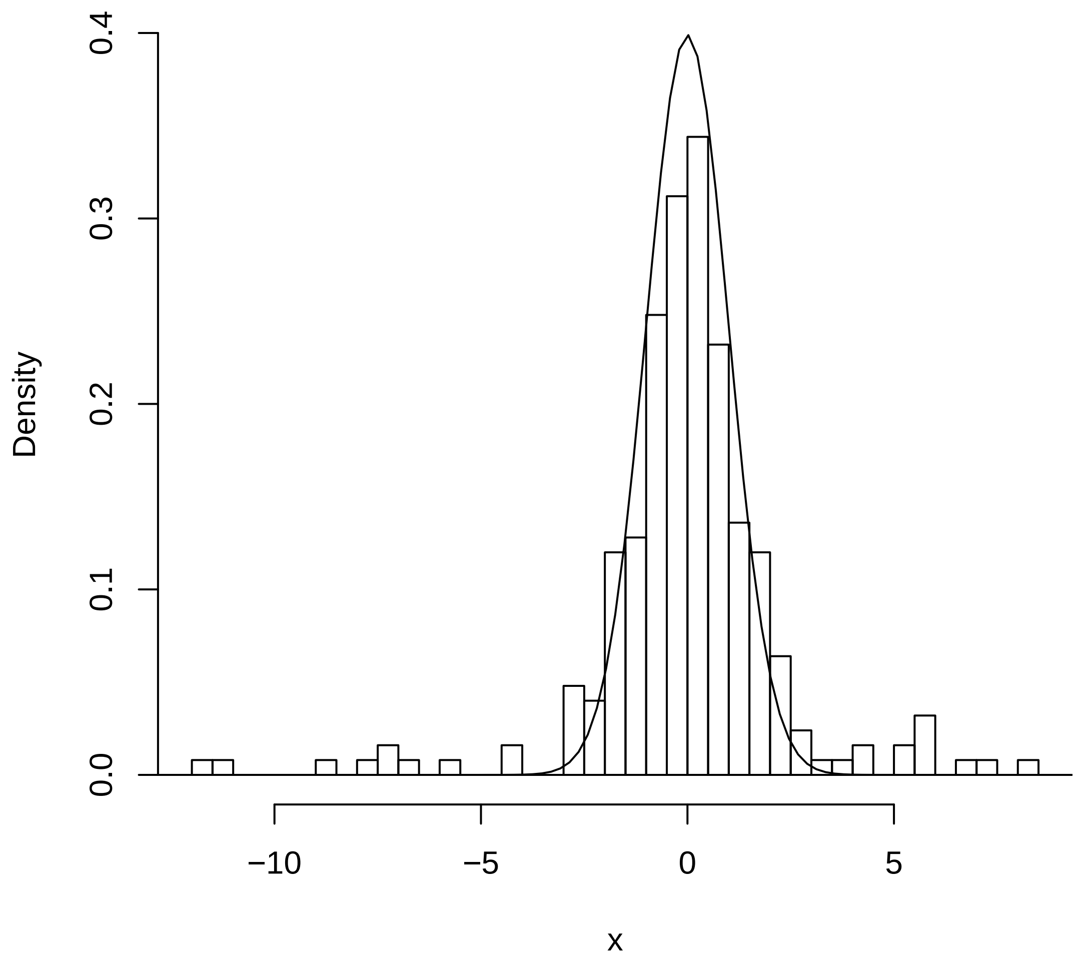
```
quercus <- read.delim("/Users/jhj1/Teaching/a192/datasets/quercus.txt", skip=24,
sep="", header=TRUE)

with(quercus, plot(tree.height[Region=="California"],
acorn.size[Region=="California"], xlab="Tree Height", pch=20, ylab="Acorn Size"))

with(quercus, points(tree.height[!Region=="California"],
acorn.size[!Region=="California"], pch=20, col="red"))

z1 <- with(quercus, lm(acorn.size[Region=="California"] ~
tree.height[Region=="California"]))

z2 <- with(quercus, lm(acorn.size[!Region=="California"] ~
tree.height[!Region=="California"]))

abline(z1)
abline(z2, col="red")

legend(22,17, c("Atlantic","California"), lty=1, col=c("black", "red"))
```


Atlantic
California
Acorn Size
Tree Height
0
5
10
15
20
25
30
0
5
10
15

Histograms

Histograms are an excellent way to explore the distributional properties of your data

```
# simulate 200 standard normal deviates
x1 <- rnorm(200)

# now another 50 with the same mean (0) but high variance
x2 <- rnorm(50,0,3)

x <- c(x1,x2)
aaa <- max(dnorm(x))

hist(x,50,freq=F,ylim=c(0,aaa), main="")
curve(dnorm(x), add=T)
```



Density
0.0
0.1
0.2
0.3
0.4
−10
−5
0
5
x

More On Histograms

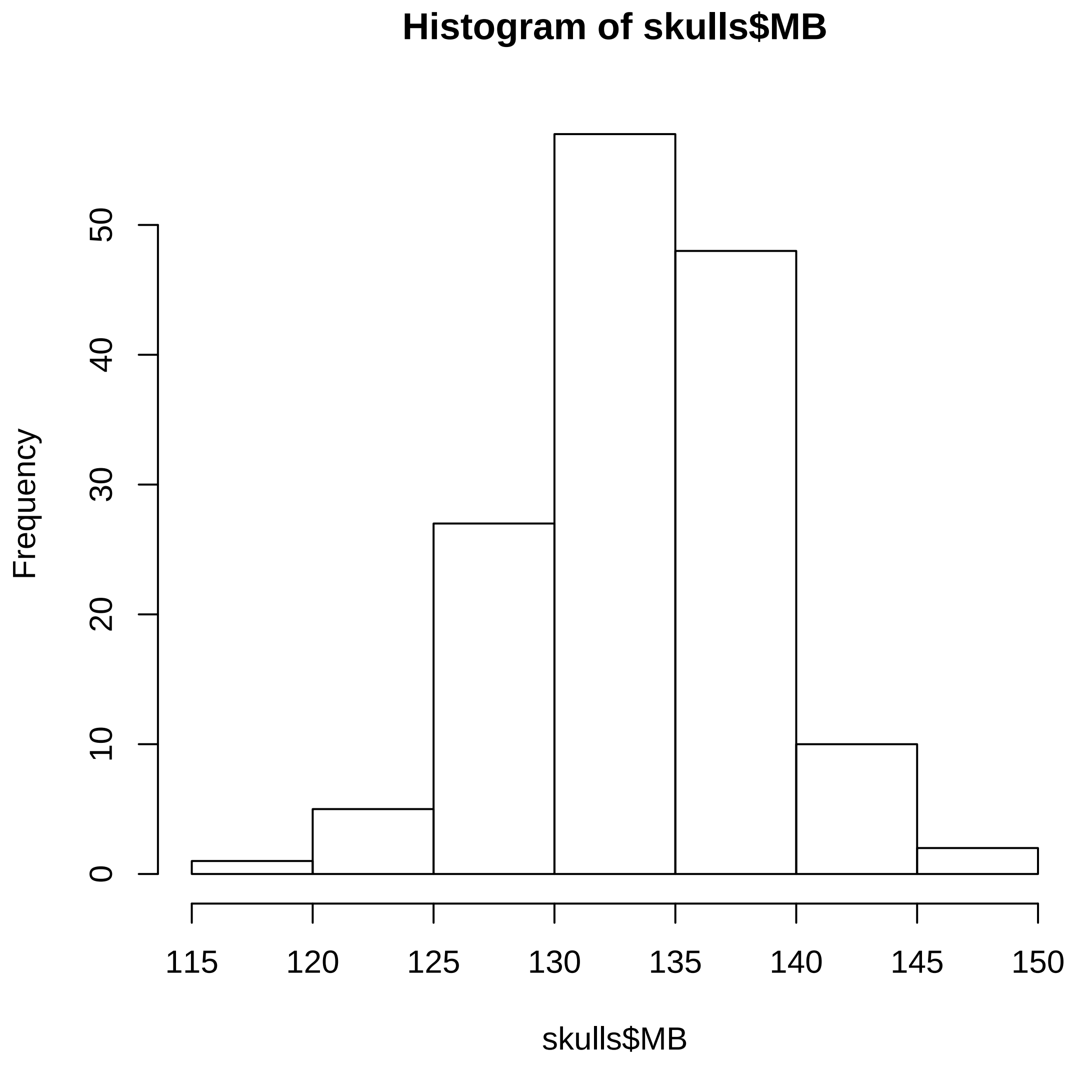
Histograms are important enough to consider them in more detail

Consider the Randall-Maciver (1905) dataset of four measurements on 150 Egyptian skulls from 4100 BP to 1755 CE

We will use a histogram to explore a bit

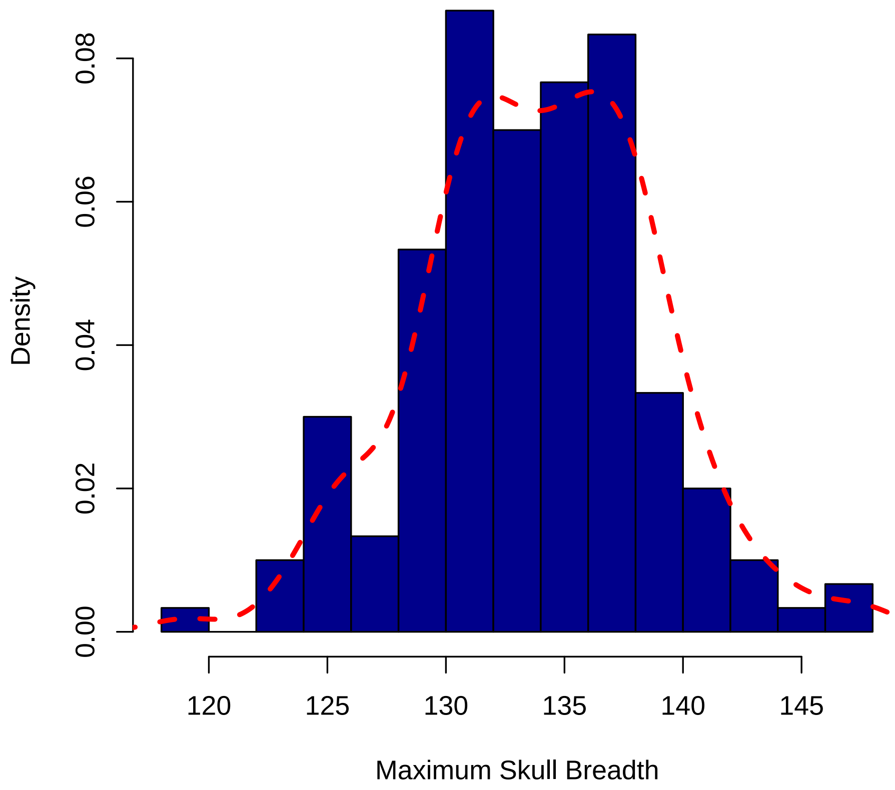
```
> skulls <- read.table("/Users/jhj1/Teaching/a192/datasets/egyptian-skulls.txt",
header=TRUE, skip=25)
> summary(skulls)
       MB               BH               BL                NH       
 Min.   :119.0   Min.   :120.0   Min.   : 81.00   Min.   :44.00  
 1st Qu.:131.0   1st Qu.:129.0   1st Qu.: 93.00   1st Qu.:49.00  
 Median :134.0   Median :133.0   Median : 96.00   Median :51.00  
 Mean   :134.0   Mean   :132.5   Mean   : 96.46   Mean   :50.93  
 3rd Qu.:137.0   3rd Qu.:136.0   3rd Qu.:100.00   3rd Qu.:53.00  
 Max.   :148.0   Max.   :145.0   Max.   :114.00   Max.   :60.00  
      Year      
 Min.   :-4000  
 1st Qu.:-3300  
 Median :-1850  
 Mean   :-1840  
 3rd Qu.: -200  
 Max.   :  150  
> hist(skulls$MB)
```

While the plot is very helpful, it doesn't look so great



Skull Histograms Continued

```
> hist(skulls$MB, 20, freq=FALSE, col="blue4", main="", xlab="Maximum Skull Breadth")
> lines(density(skulls$MB), lty=2,lwd=3, col="red")
```



What I Done

What did I do here?

First, I changed the number of bins that the histogram uses with the second argument (i.e., 20)

Changed it from a frequency histogram to an probability histogram using `freq=FALSE` (Why would I do such a thing?)

Colored the bars with a nice blue, `col=blue4`

Suppressed the title (`main=""`) and labeled the abscissa with something meaningful (`xlab="Maximum Skull Breadth"`)

Finally, I used a kernel density estimator to draw a non-parametric estimate of the probability density given by this histogram (this is why I used the `freq=FALSE` argument)

I used the `lines()` command, which is a way of adding a line to an existing plot, to add the density estimator

The argument `lty=2` makes the line dashed and the argument `lwd=3` made the line width 3 pixels (if on a computer screen) or 2.25 points on a pdf graphics device

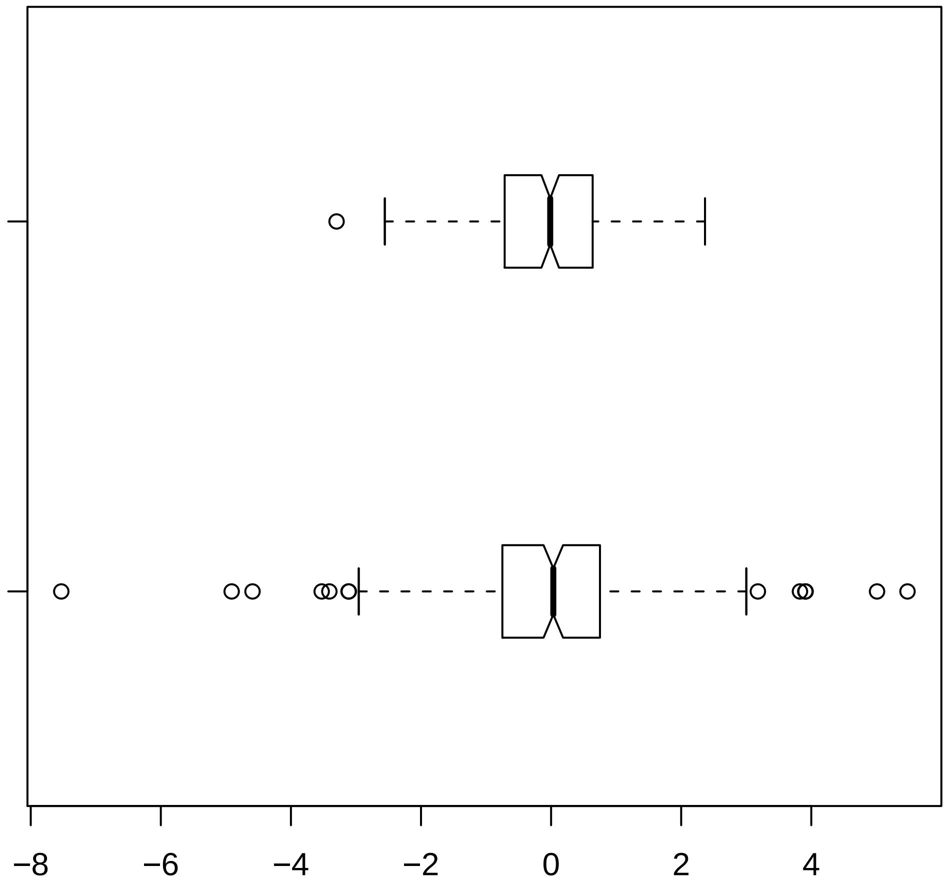
This density is rather suggestive that we might have a mixture of multiple populations in this sample because of its pronounced bimodality

Boxplots

Boxplots give a handy way of exploring the distribution of a sample and of comparing two (or more) samples

Creating a boxplot of the contaminated sample and comparing to an uncontaminated sample gives more weight to the hypothesis that the tails of our contaminated sample are too heavy

```
> boxplot(x,y,notch=T,horizontal=T, boxwex=.25)
```


−8
−6
−4
−2
0
2
4

Plotting Expressions

Sometimes you just want to plot a mathematical function

Use `expression()` to set up a function to plot

`expression()` basically says here's something to calculate, but wait until I tell you to do wo with `eval()`

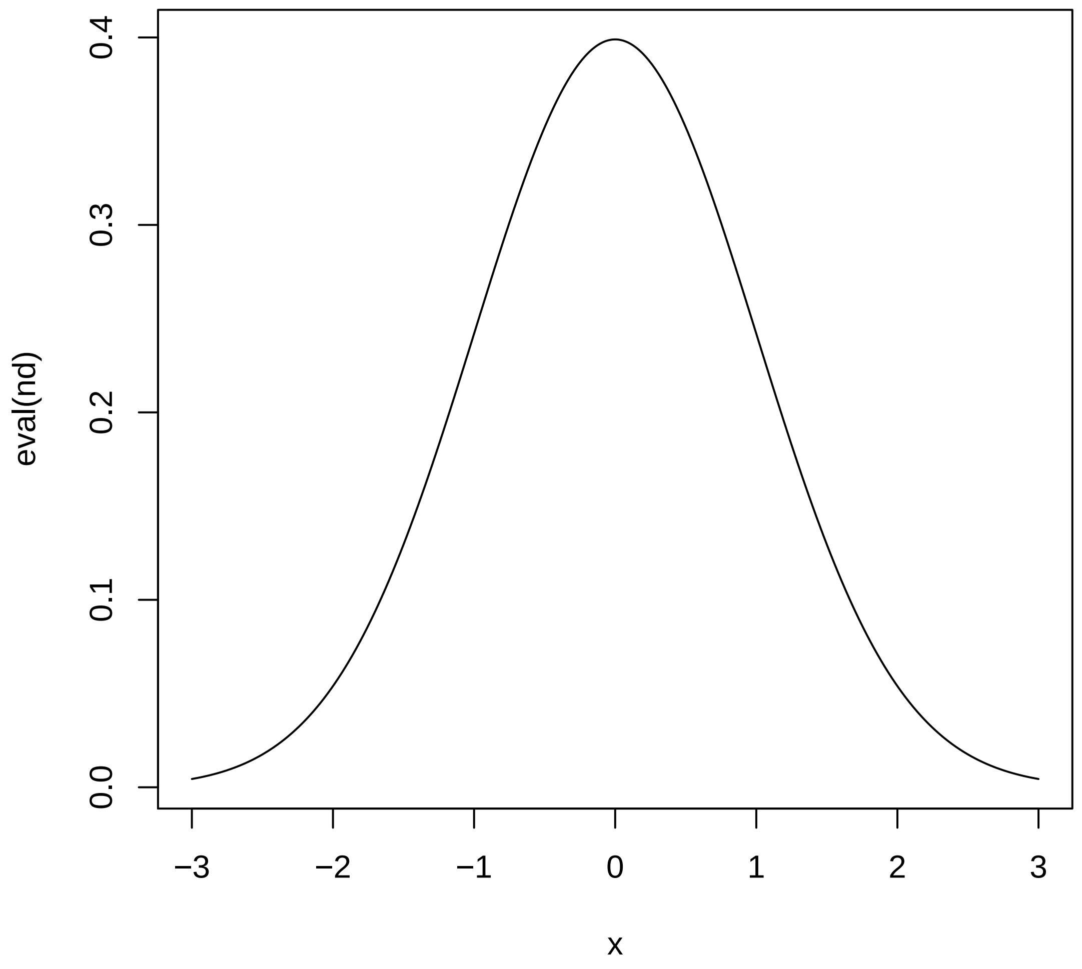
Calculation are, of course, vectorized

Don't overdo this one – it has its place, but is rather limited

Plot a normal density the hard way

```
> nd <- expression((1/sqrt(2*pi*sigma2))*exp(-(x-mu)^2/(2*sigma2)))
> x <- seq(-3,3,length=1000)
> plot(x,eval(nd), type="l")
```

In reality, you'd use `dnorm()` to plot this curve


eval(nd)
0.0
0.1
0.2
0.3
0.4
−3
−2
−1
0
1
2
3
x

Sourcing Code

When you have many commands that you need to execute to perform an analysis or create a graphic, it is often convenient to collect those commands into an R script

Call a script using the command `source()`

Take the example of fitting the logistic model to the USA population series 1790-1930

We need to fit a model with two parameters and do so using nonlinear least-squares minimization

```
> usa <- scan("/Users/jhj1/Teaching/summercourse/rdemog/usa.txt")
Read 21 items
> usa
 [1]   3.929214   5.308483   7.239881   9.638453  12.866020  17.866020
 [7]  23.191876  31.443321  38.558371  50.189209  62.979766  76.212168
[13]  92.228496 106.021537 123.202624 132.164569 151.325798 179.323175
[19] 203.302031 226.542199 248.709873
> year <- seq(1790,1990,by=10)
> year1 <- year[1:15]
> usa1 <- usa[1:15]
> logistic.int <- expression(n0 * exp(p[1] * t)/(1 + n0 * (exp(p[1] *
t) - 1)/p[2]))
```

```
> r.guess <- (log(usa1[15])-log(usa1[1]))/140
> r.guess
[1] 0.02460994
> k.guess <- usa1[15]
> par <- c(r.guess,k.guess)
> source("/Users/jhj1/Teaching/summercourse/rdemog/fit.logistic.r")
> usa1930.fit <- optim(par,fit.logistic,y=usa1)
> usa1930.fit
$par
[1]   0.03126429 198.61573375

$value
[1] 4.830198

$counts
function gradient
     193       NA

$convergence
[1] 0

$message
NULL
```

Another Example

Say we want to look at the sex-specific scaling of body mass with height

Use data from NHANES

Produce a scatter plot of body mass vs. stature

Fit smooth curves for males and females separately

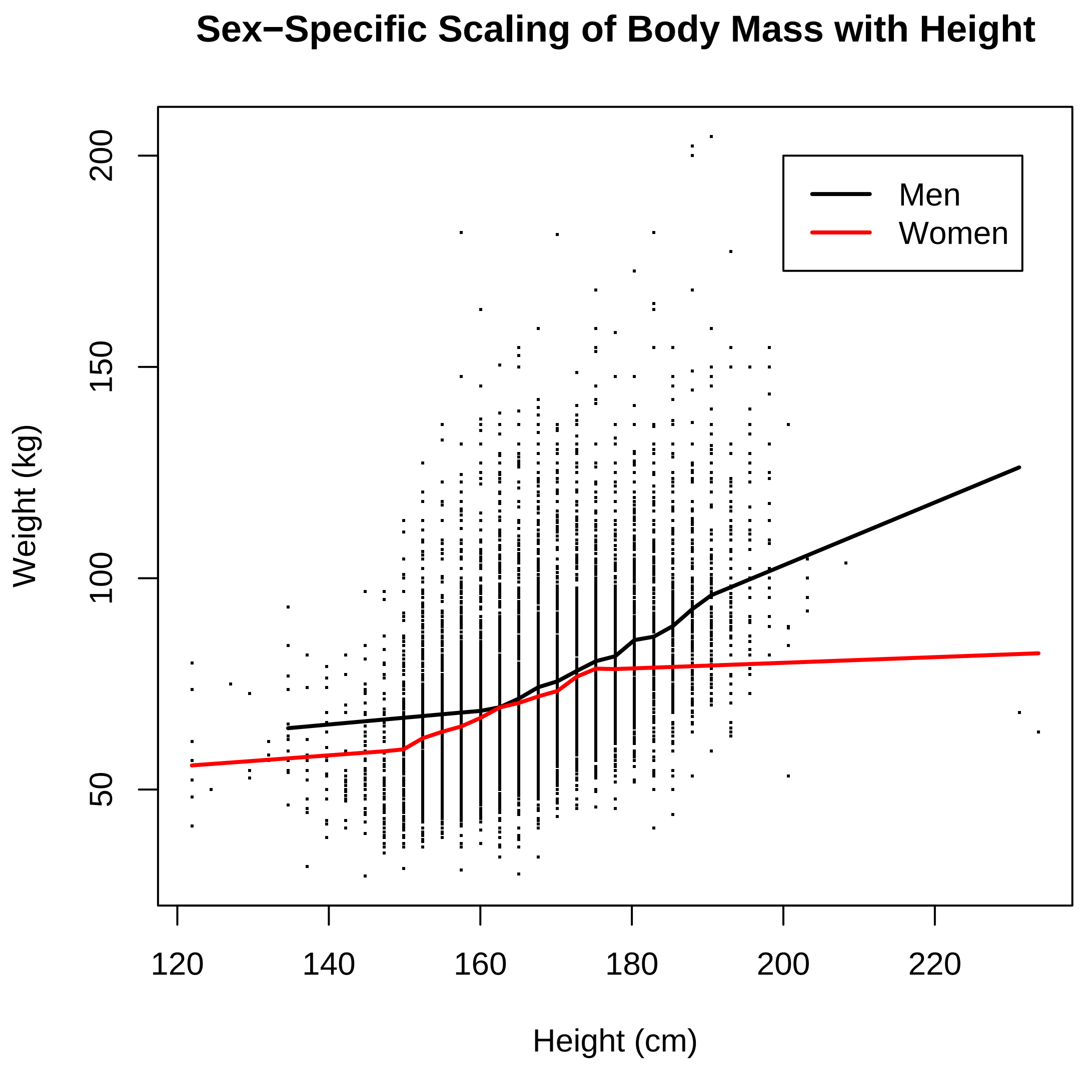
Here is a script to produce the plot – enter and save this using a text editor:

```
# Plots body mass (kg) against stature (cm) for 18,648 complete
# observations from the NHANES data
# draws Friedman's super smoother curves for males and females

# data already extracted from NHANES and saved as a binary file
load("body.size.RData")

# get rid of NAs so supsmu doesn't shoot out warnings
cheight <- !is.na(body.size$height)
cweight <- !is.na(body.size$weight)
height <- body.size$height[cheight & cweight]
weight <- body.size$weight[cheight & cweight]
```

```
sex <- body.size$sex[cheight & cweight]

# convert to metric!
plot(height*2.54,weight/2.2, pch=".", xlab="Height (cm)", ylab="Weight (kg)")
lines(supsmu(2.54*height[sex==1],weight[sex==1]/2.2),lwd=2)
lines(supsmu(2.54*height[sex==2],weight[sex==2]/2.2),lwd=2, col="red")
legend(200,200, c("Men", "Women"), lwd=2, col=c("black", "red"))
title("Sex-Specific Scaling of Body Mass with Height")
```

Now source the code

```
> source("make.demo.plot.r")
```


Sex−Specific Scaling of Body Mass with Height
Weight (kg)
Height (cm)
Men
Women
50
100
150
200
120
140
160
180
200
220